

CRF Errors Edited by the STIC Systems Branch

Serial Number: 10/759,037A

CRF Edit Date: 3/29/05
Edited by: AC

- Realigned nucleic acid/amino acid numbers/text in cases where the sequence text "wrapped" to the next line
- Corrected the SEQ ID NO. Sequence numbers edited were:

- Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

Deleted: invalid beginning/end-of-file text ; page numbers

- Inserted mandatory headings/numeric identifiers, specifically:

- Moved responses to same line as heading/numeric identifier, specifically:

- Other:



IFW16

RAW SEQUENCE LISTING

DATE: 03/29/2005

PATENT APPLICATION: US/10/759,037A.

TIME: 12:42:39

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\03292005\J759037A.raw

3 <110> APPLICANT: Yosef, Shaul
 4 Zemel, Romi
 6 <120> TITLE OF INVENTION: HEPATITIS B VIRUS BINDING PROTEINS AND USES THEREOF
 8 <130> FILE REFERENCE: 27169
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/759,037A
 C--> 10 <141> CURRENT FILING DATE: 2004-01-20
 10 <160> NUMBER OF SEQ ID NOS: 14
 12 <170> SOFTWARE: PatentIn version 3.3
 14 <210> SEQ ID NO: 1
 15 <211> LENGTH: 2512
 16 <212> TYPE: DNA
 17 <213> ORGANISM: Homo sapiens
 19 <400> SEQUENCE: 1
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 22 tgtgacattg tcccagacgc ttgttaaagggt ggaatgaagt gtgtcaacca ctatggagga 120
 24 tacctctgcc ttccgaaaac agcccagatt attgtcaata atgaacagcc tcagcaggaa 180
 26 acacaaccag cagaaggAAC ctcaggggca accacgggg ttgttagctgc cagcagcatg 240
 28 gcaaccagtg gagtgtgcc cgggggtggg tttgtggcca gtgtctgtc agtgcgcaggc 300
 30 cctgaaatgc agactggccg aaataacttt gtcatccggc ggaacccagc tgaccctcg 360
 32 cgcattccct ccaacccttc ccaccgtatc cagtgtcagc caggctacga gcaaagtgaa 420
 34 cacaacgtgt gccaagacat agacgagtgc actgcaggga cgcacaactg tagagcagac 480
 36 caagtgtgca tcaatttacg gggatccttt gcatgtcagt gccctcctgg atatcagaag 540
 38 cgagggggc agtgcgtaga catagatgaa tgtacatcc ctccatattt ccaccaaaga 600
 40 tgcgtgataa caccaggctc attttattgc cagtgcgtc ctgggttca attggcagca 660
 42 aacaactata cctgcgtaga tataaatgaa tgtatgtcc gcaatcaatg tgctcagcag 720
 44 tgctacaaca ttcttggttc attcatctgt cagtgcatac aaggatatga gctaagcagt 780
 46 gacaggctca actgtgaaga cattgtgaa tgcagaacct caagctacat gtgtcaatat 840
 48 caatgtgtca atgaacctgg gaaattctca tgtatgtgcc cccagggata ccaagtgggt 900
 50 agaagttagaa catgtcaaga tataaatgag tgtgagacca caaatgaatg ccgggaggat 960
 52 gaaatgtgtt ggaattatca tggcggcttc cggtttatc cacgaaatcc ttgtcaagat 1020
 54 ccctacattc taacaccaga gaaccgatgt gtttgcctc tctcaaattgc catgtgccga 1080
 56 gaactgcccc agtcaatagt ctacaaatac atgagcatcc gatctgatag gtctgtgcc 1140
 58 tcagacatct tccagataca gcccacaact atttatgcca acaccatcaa tactttcg 1200
 60 attaaatctg gaaataaaaa tggaggttc tacctacgac aaacaagtcc tgtaagtgca 1260
 62 atgcttgtc tcgtgaagtc attatcagga ccaagagaac atatcgtgga cctggagatg 1320
 64 ctgacagtca gcagtatagg gaccttccgc acaagctctg tgttaagatt gacaataata 1380
 66 gtggggccat tttcatttta gtctttctta agagtcaccc acaggcattt aagtcagcca 1440
 68 aagaatattg ttacctaaa gcaactatTTT atttatagat atatctgtc catctacatc 1500
 70 tctatactgt acactcaccc ataacaaaca attacaccat ggtataaaatg gggcattaa 1560
 72 tatgtaaaga ttcaaagttt gtcttttatta ctatatgtaa attagacatt aatccactaa 1620
 74 actgggtcttc ttcaagagag ctaagtatac actatctggt gaaacttgga ttcttccta 1680
 76 taaaagtggg accaagcaat gatgtatcc tgcgtgtcatt aaggaaactt actagagctc 1740
 78 cactaacagt ctcataagga ggcagccatc ataaccattt aatagcatgc aagggtaa 1800

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80 atgagtttt aactgcttg taagaaaatg gaaaaggtaa ataaagatat atttcttag 1860
82 aaaatggga tctgccatat ttgtgttggg ttttattttc atatccagcc taaaggtgg 1920
84 tggtttattat atagtaataa atcattgctg tacaacatgc tggtttctgt agggtat 1980
86 taatttgtc agaaatttaa gattgtgaat atttgtaaa aaacagtaag caaaatttc 2040
88 cagaattccc aaaatgaacc agataccccc tagaaaatta tactattgag aaatctatgg 2100
90 ggaggatatg agaaaataaa ttcccttctaa accacattgg aactgacctg aagaagcaaa 2160
92 ctcggaaaat ataataacat ccctgaattc aggcatc aagatgcaga acaaaatgg 2220
94 taaaaggtat ttcaactggg aagtttaat ttcttaagtaa aatttaaattc ctaacacttc 2280
96 actaatttt aactaaaatt totcatcttc gtacttgatg ctcacagagg aagaaaatga 2340
98 tggatgtttt tattcctggc atccagagtg acagtgaact taagcaaatt accctcctac 2400
100 ccaattctat ggaatatttt atacgtctcc ttgtttaaaa tctgactgct ttactttgat 2460
102 gtatcatatt tttaaataaaa aataaatatt cctttagaag atcactctaa aa 2512
105 <210> SEQ ID NO: 2
106 <211> LENGTH: 387
107 <212> TYPE: PRT
108 <213> ORGANISM: Homo sapiens
110 <400> SEQUENCE: 2
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113 1 5 10 15
116 Ala Ala Val Ala Gly Pro Glu Met Gln Thr Gly Arg Asn Asn Phe Val
117 20 25 30
120 Ile Arg Arg Asn Pro Ala Asp Pro Gln Arg Ile Pro Ser Asn Pro Ser
121 35 40 45
124 His Arg Ile Gln Cys Ala Ala Gly Tyr Glu Gln Ser Glu His Asn Val
125 50 55 60
128 Cys Gln Asp Ile Asp Glu Cys Thr Ala Gly Thr His Asn Cys Arg Ala
129 65 70 75 80
132 Asp Gln Val Cys Ile Asn Leu Arg Gly Ser Phe Ala Cys Gln Cys Pro
133 85 90 95
136 Pro Gly Tyr Gln Lys Arg Gly Glu Gln Cys Val Asp Ile Asp Glu Cys
137 100 105 110
140 Thr Ile Pro Pro Tyr Cys His Gln Arg Cys Val Asn Thr Pro Gly Ser
141 115 120 125
144 Phe Tyr Cys Gln Cys Ser Pro Gly Phe Gln Leu Ala Ala Asn Asn Tyr
145 130 135 140
148 Thr Cys Val Asp Ile Asn Glu Cys Asp Ala Ser Asn Gln Cys Ala Gln
149 145 150 155 160
152 Gln Cys Tyr Asn Ile Leu Gly Ser Phe Ile Cys Gln Cys Asn Gln Gly
153 165 170 175
156 Tyr Glu Leu Ser Ser Asp Arg Leu Asn Cys Glu Asp Ile Asp Glu Cys
157 180 185 190
160 Arg Thr Ser Ser Tyr Leu Cys Gln Tyr Gln Cys Val Asn Glu Pro Gly
161 195 200 205
164 Lys Phe Ser Cys Met Cys Pro Gln Gly Tyr Gln Val Val Arg Ser Arg
165 210 215 220
168 Thr Cys Gln Asp Ile Asn Glu Cys Glu Thr Thr Asn Glu Cys Arg Glu
169 225 230 235 240
172 Asp Glu Met Cys Trp Asn Tyr His Gly Gly Phe Arg Cys Tyr Pro Arg
173 245 250 255

RAW SEQUENCE LISTING DATE: 03/29/2005
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Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF4\03292005\J759037A.raw

176 Asn Pro Cys Gln Asp Pro Tyr Ile Leu Thr Pro Glu Asn Arg Cys Val
177 260 265 270
180 Cys Pro Val Ser Asn Ala Met Cys Arg Glu Leu Pro Gln Ser Ile Val
181 275 280 285
184 Tyr Lys Tyr Met Ser Ile Arg Ser Asp Arg Ser Val Pro Ser Asp Ile
185 290 295 300
188 Phe Gln Ile Gln Ala Thr Thr Ile Tyr Ala Asn Thr Ile Asn Thr Phe
189 305 310 315 320
192 Arg Ile Lys Ser Gly Asn Glu Asn Gly Glu Phe Tyr Leu Arg Gln Thr
193 325 330 335
196 Ser Pro Val Ser Ala Met Leu Val Leu Val Lys Ser Leu Ser Gly Pro
197 340 345 350
200 Arg Glu His Ile Val Asp Leu Glu Met Leu Thr Val Ser Ser Ile Gly
201 355 360 365
204 Thr Phe Arg Thr Ser Ser Val Leu Arg Leu Thr Ile Ile Val Gly Pro
205 370 375 380
208 Phe Ser Phe
209 385
212 <210> SEQ ID NO: 3
213 <211> LENGTH: 2019
214 <212> TYPE: DNA
215 <213> ORGANISM: Homo sapiens
218 <220> FEATURE:
219 <221> NAME/KEY: misc_feature
220 <222> LOCATION: (22)..(22)
221 <223> OTHER INFORMATION: n is a, c, g, or t
223 <400> SEQUENCE: 3

W--> 224	accccgccgc	tctccccgtg	tnctctccac	gactcgctcg	gccccctctgg	aataaaacac	60
226	cccgagcccc	cgagggccca	gaggaggccg	acgtccccga	gctcctccgg	gggtcccgcc	120
228	cgcagaagctt	cttctcgccct	tcgcacatctcc	tcctcgcgcg	tcttggacat	gccagaata	180
230	aaaaggatac	tcactgttac	cattctggct	ctctgttcc	caagccctgg	aatgcacag	240
232	gcacagtgc	cgaatggctt	tgacactggat	cgccagtcag	gacagtgttt	agatattgat	300
234	gaatgccgaa	ccatccccga	ggcctgcccga	ggagacatga	tgtgtgttaa	ccaaaatggg	360
236	gggtattttat	gccattcccc	gacaaaacct	gtgtatcgag	ggccctactc	gaaccctac	420
238	tcgacccccc	actcagggtcc	gtacccagca	gctgccccac	cactctcagc	tccaaactat	480
240	cccacgatct	ccaggccctct	tatatgccgc	tttggatacc	agatggatga	aagcaaccaa	540
242	tgtgtggatg	tggacgagtg	tgcaacagat	tcccaccagt	gcaaccccccac	ccagatttgc	600
244	atcaatatga	agggcgggta	cacctgctcc	tgcacccgacg	gatattggct	tttggaaaggc	660
246	cagtgccttag	acattgtatga	atgtcgctat	ggttactgcc	agcagctctg	tgcgaatgtt	720
248	cctggatcct	attcttgtac	atgcaacccct	ggttttaccc	tcaatgagga	ttgaaggct	780
250	tgccaagatg	tgaacgagtg	tgcaccccgag	aaccctgcg	tgc当地acacc	cgtcaacacc	840
252	tacgctctt	tcatctggcc	ctgtgaccca	ggatataaac	ttgaggaaga	ttggcgttcat	900
254	tgcagtgata	tggacgagtg	cagttctct	gagttcctct	gccaacatga	gtgtgtgaac	960
256	cagccggca	catacttctg	ctcctgccc	ccaggctaca	tcctgctgga	tgacaaccga	1020
258	agctgccaag	acatcaacga	atgtgagcac	aggaaccaca	cgtgcaaccc	gcagcagacg	1080
260	tgctacaatt	tacaaggggg	cttcaaattgc	atcgacccca	tccgctgtga	ggagccttat	1140
262	ctgaggatca	gtgataaccg	ctgtatgtgt	cctgctgaga	accctggctg	cagagaccag	1200
264	ccctttacca	tcttgtaccg	ggacatggac	gtgggtcag	gacgctccgt	tcccgtgac	1260
266	atcttccaaa	tgcaagccac	gaccgctac	cctggggcct	attacatttt	ccagatcaaa	1320

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268 tctggaaatg agggcagaga atttacatg cggcaaacgg gccccatcag tgccaccctg 1380
 270 gtatgacac gccccatcaa agggcccccgg gaaatccagc tggacttggaa aatgatcact 1440
 272 gtcaacactg tcataactt cagaggcagc tccgtatcc gactgcggat atatgtgtcg 1500
 274 cagtacccat tctgagcctc gggctggagc ctccgacgct gcctctcatt ggcaccaagg 1560
 276 gacaggagaa gagagaaat aacagagaga atgagagcga cacagacgtt aggcatattcc 1620
 278 tgctgaacgt ttccccgaag agtcagcccc gacttcctga ctctcacctg tactattgca 1680
 280 gacctgtcac cctgcaggac ttgccacccc cagttctat gacacagttt tcaaaaaagta 1740
 282 ttatcattgc tcccctgata gaagattttt ggttaattttt caaggccttc agtttatttc 1800
 284 cactattttc aaagaaaata gattagttt gcgggggtct gagtctatgt tcaaagactg 1860
 286 tgaacagctt gctgtcaattt cttcacctt tccactcctt ctctcacgtt gttactgtt 1920
 288 tgcaaagacc cggggagctg gcggggaaac cctggggagt agctagttt cttttgcgt 1980
 290 acacagaaga aggctatgtt aacaaaccac agcaggatc 2019
 293 <210> SEQ ID NO: 4
 294 <211> LENGTH: 448
 295 <212> TYPE: PRT
 296 <213> ORGANISM: Homo sapiens
 298 <400> SEQUENCE: 4
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 304 Leu Pro Ser Pro Gly Asn Ala Gln Ala Gln Cys Thr Asn Gly Phe Asp
 305 20 25 30
 308 Leu Asp Arg Gln Ser Gly Gln Cys Leu Asp Ile Asp Glu Cys Arg Thr
 309 35 40 45
 312 Ile Pro Glu Ala Cys Arg Gly Asp Met Met Cys Val Asn Gln Asn Gly
 313 50 55 60
 316 Gly Tyr Leu Cys His Ser Arg Thr Asn Pro Val Tyr Arg Gly Pro Tyr
 317 65 70 75 80
 320 Ser Asn Pro Tyr Ser Thr Pro Tyr Ser Gly Pro Tyr Pro Ala Ala Ala
 321 85 90 95
 324 Pro Pro Leu Ser Ala Pro Asn Tyr Pro Thr Ile Ser Arg Pro Leu Ile
 325 100 105 110
 328 Cys Arg Phe Gly Tyr Gln Met Asp Glu Ser Asn Gln Cys Val Asp Val
 329 115 120 125
 332 Asp Glu Cys Ala Thr Asp Ser His Gln Cys Asn Pro Thr Gln Ile Cys
 333 130 135 140
 336 Ile Asn Met Lys Gly Gly Tyr Thr Cys Ser Cys Thr Asp Gly Tyr Trp
 337 145 150 155 160
 340 Leu Leu Glu Gly Gln Cys Leu Asp Ile Asp Glu Cys Arg Tyr Gly Tyr
 341 165 170 175
 344 Cys Gln Gln Leu Cys Ala Asn Val Pro Gly Ser Tyr Ser Cys Thr Cys
 345 180 185 190
 348 Asn Pro Gly Phe Thr Leu Asn Glu Asp Gly Arg Ser Cys Gln Asp Val
 349 195 200 205
 352 Asn Glu Cys Ala Thr Glu Asn Pro Cys Val Gln Thr Cys Val Asn Thr
 353 210 215 220
 356 Tyr Gly Ser Phe Ile Cys Arg Cys Asp Pro Gly Tyr Glu Leu Glu Glu
 357 225 230 235 240
 360 Asp Gly Val His Cys Ser Asp Met Asp Glu Cys Ser Phe Ser Glu Phe
 361 245 250 255

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364 Leu Cys Gln His Glu Cys Val Asn Gln Pro Gly Thr Tyr Phe Cys Ser
 365 260 265 270
 368 Cys Pro Pro Gly Tyr Ile Leu Leu Asp Asp Asn Arg Ser Cys Gln Asp
 369 275 280 285
 372 Ile Asn Glu Cys Glu His Arg Asn His Thr Cys Asn Leu Gln Gln Thr
 373 290 295 300
 376 Cys Tyr Asn Leu Gln Gly Gly Phe Lys Cys Ile Asp Pro Ile Arg Cys
 377 305 310 315 320
 380 Glu Glu Pro Tyr Leu Arg Ile Ser Asp Asn Arg Cys Met Cys Pro Ala
 381 325 330 335
 384 Glu Asn Pro Gly Cys Arg Asp Gln Pro Phe Thr Ile Leu Tyr Arg Asp
 385 340 345 350
 388 Met Asp Val Val Ser Gly Arg Ser Val Pro Ala Asp Ile Phe Gln Met
 389 355 360 365
 392 Gln Ala Thr Thr Arg Tyr Pro Gly Ala Tyr Tyr Ile Phe Gln Ile Lys
 393 370 375 380
 396 Ser Gly Asn Glu Gly Arg Glu Phe Tyr Met Arg Gln Thr Gly Pro Ile
 397 385 390 395 400
 400 Ser Ala Thr Leu Val Met Thr Arg Pro Ile Lys Gly Pro Arg Glu Ile
 401 405 410 415
 404 Gln Leu Asp Leu Glu Met Ile Thr Val Asn Thr Val Ile Asn Phe Arg
 405 420 425 430
 408 Gly Ser Ser Val Ile Arg Leu Arg Ile Tyr Val Ser Gln Tyr Pro Phe
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 412 <210> SEQ ID NO: 5
 413 <211> LENGTH: 1661
 414 <212> TYPE: DNA
 415 <213> ORGANISM: Homo sapiens
 417 <400> SEQUENCE: 5
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 422 gatggctata cccagacagc caactgcggg gatgtcaacg agtgtctgac catccctgag 180
 424 gcctgcaagg gggaaatgaa gtgcataaac cactacgggg gctacttgt cctgccccgc 240
 426 tccgctgccc tcataaacga cctacacggc gagggacccc cgccaccagt gcctcccg 300
 428 aacacccaac ccctgcccac aggctatgag cccgacgatc aggacagctg tgtggatgtg 360
 430 gacgagtgtg cccaggccct gcacgactgt cgccccagcc aggactgcca taactgcct 420
 432 ggctcctatc agtgcacctg ccctgatggt taccgcaaga tcgggcccga gtgtgtggac 480
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 436 cgctgcccagt gcgagccggg ttccagctg gggctctaaca accgctctg tggatgtg 600
 438 aacgagtgtg acatgggggc cccatgcgag cagcgctgt tcaactccta tggacatcc 660
 440 ctgtgtcgct gccaccaggc ctatgagctg catcggtatc gcttctctg cagtatatt 720
 442 gatgagtgtt gctaactccag ctacccatgt cagtaccgtc gctcaacga gccaggccgt 780
 444 ttctccctgcc actgcccaca gggttaccag ctgcgtggcca cacgcctctg ccaagacatt 840
 446 gatgagtgtg agtctgggtc gcaccaggatc tccgaggccc aaacctgtt caattccat 900
 448 gggggctacc gctgcgttga caccaaccgc tgcgtggagc cctacatcca ggtctctgag 960
 450 aaccgctgtc tctgcggcgc ctccaaacct ctatgtcgag agcagccctc atccattgtg 1020
 452 caccgctaca tgaccatcac ctgcggaaagcg gagagacccg ctgacgtgtt ccagatccag 1080
 454 gcgacctccg tctaccggg tgcctacaat gccttcaga tccgtgttgc aaactcgac 1140
 456 ggggactttt acattaggca aatcaacaac gtcagcgcca tgctggctc cgcccgccg 1200

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; N Pos. 22/

VERIFICATION SUMMARY

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L:10 M:270 C: Current Application Number differs, Replaced Current Application No

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:224 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0